

1600

RAW SEQUENCE LISTING

DATE: 07/21/2003

PATENT APPLICATION: US/09/857,583A

TIME: 09:49:11

Input Set : N:\Crf4\Refhold\I857583.raw

Output Set: N:\CRF4\07212003\I857583A.raw

1 <110> APPLICANT: Browse, John et al.  
 2 <120> TITLE OF INVENTION: DESATURASES AND METHODS OF USING THEM FOR SYNTHESIS OF  
 POLYUNSATURATED

3 FATTY ACIDS

4 <130> FILE REFERENCE: 4630-58963

5 <140> CURRENT APPLICATION NUMBER: US/09/857,583A

6 <141> CURRENT FILING DATE: 2001-08-17

7 <150> PRIOR APPLICATION NUMBER: US 60/111,301

8 <151> PRIOR FILING DATE: 1998-12-07

9 <150> PRIOR APPLICATION NUMBER: PCT/US99/28655

10 <151> PRIOR FILING DATE: 1999-12-06

11 <160> NUMBER OF SEQ ID NOS: 13

12 <170> SOFTWARE: PatentIn version 3.1

14 <210> SEQ ID NO: 1

15 <211> LENGTH: 1461

16 <212> TYPE: DNA

17 <213> ORGANISM: Caenorhabditis elegans

18 <400> SEQUENCE: 1

19	gaattttcaa	tctctcttgg	gtcccaccgc	tgtgatataca	aaatgggtatt	acgagagcaa	60
20	gagcatgagc	cattcttcat	taaaattgat	ggaaaatggt	gtcaaattga	cgatgctgtc	120
21	ctgagatcac	atccaggtgg	tagtgcaatt	actacctata	aaaatatgga	tgccactacc	180
22	gtattccaca	cattccatac	tggttctaaa	gaagcgtatc	aatgggtgac	agaattgaaa	240
23	aaagagtgcc	ctacacaaga	accagagatc	ccagatatta	aggatgaccc	aatcaaagga	300
24	attgatgatg	tgaacatggg	aactttcaat	atttctgaga	aacgatctgc	ccaaataaat	360
25	aaaagtttca	ctgatctacg	tatgcgagtt	cgtgcagaag	gacttatgga	tggatctcct	420
26	ttgttctaca	ttagaaaaat	tcttgaaaca	atcttcacaa	ttctttttgc	attctacctt	480
27	caataccaca	catattatct	tccatcagct	attctaattg	gagttgcgtg	gcaacaattg	540
28	ggatgggttaa	tccatgaatt	cgcacatcat	cagttgttca	aaaacagata	ctacaatgat	600
29	ttggccagct	atttcgttgg	aaacttttta	caaggattct	catctgggtg	ttggaaagag	660
30	cagcacaatg	tgcatacgc	agccacaaat	gttgttggac	gagacggaga	tcttgattta	720
31	gtcccattct	atgetacagt	ggcagaacat	ctcaacaatt	attctcagga	ttcatgggtt	780
32	atgactctat	tcagatggca	acatgttcat	tggacattca	tgttaccatt	cctccgtctc	840
33	tcgtggcttc	ttcagtcaat	catttttgtt	agtcagatgc	caactcatta	ttatgactat	900
34	tacagaaata	ctgcgattta	tgaacagggt	ggctctctct	tgcactgggc	ttggtcattg	960
35	ggccaattgt	atttctctacc	cgattgggtca	actagaataa	tgttcttctt	tgtttctcat	1020
36	cttgattggag	gtttcctgct	ctctcatgta	gttactttca	atcattattc	agtggagaag	1080
37	tttgattgga	gctcgaacat	catgtcaaat	tacgcttgtc	ttcaaatcat	gaccacaaga	1140
38	aatatgagac	ctggaagatt	cattgactgg	ctttggggag	gtcttaacta	tcagattgag	1200
39	caccatcttt	tcccaacgat	gccacgacac	aacttgaaca	ctgttatgcc	acttgtaaag	1260
40	gagtttgag	cagcaaatgg	tttaccatac	atggtcgacg	attatttcac	aggattctgg	1320
41	cttgaaattg	agcaattccg	aaatattgca	aatgttgctg	ctaaattgac	taaaaagatt	1380
42	gcctagatta	cgattaatta	atcaatttat	tttcatgttc	tattcgtgtg	ttttaatatt	1440
43	ttccaaattt	ttacctattc	c				1461

45 <210> SEQ ID NO: 2

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Input Set : N:\Crif4\Refhold\I857583.raw

Output Set: N:\CRF4\07212003\I857583A.raw

46 &lt;211&gt; LENGTH: 447

47 &lt;212&gt; TYPE: PRT

48 &lt;213&gt; ORGANISM: Caenorhabditis elegans

49 &lt;400&gt; SEQUENCE: 2

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50 Met Val Leu Arg Glu Gln Glu His Glu Pro Phe Phe Ile Lys Ile Asp
51 1 5 10 15
52 Gly Lys Trp Cys Gln Ile Asp Asp Ala Val Leu Arg Ser His Pro Gly
53 20 25 30
54 Gly Ser Ala Ile Thr Thr Tyr Lys Asn Met Asp Ala Thr Thr Val Phe
55 35 40 45
56 His Thr Phe His Thr Gly Ser Lys Glu Ala Tyr Gln Trp Leu Thr Glu
57 50 55 60
58 Leu Lys Lys Glu Cys Pro Thr Gln Glu Pro Glu Ile Pro Asp Ile Lys
59 65 70 75 80
60 Asp Asp Pro Ile Lys Gly Ile Asp Asp Val Asn Met Gly Thr Phe Asn
61 85 90 95
62 Ile Ser Glu Lys Arg Ser Ala Gln Ile Asn Lys Ser Phe Thr Asp Leu
63 100 105 110
64 Arg Met Arg Val Arg Ala Glu Gly Leu Met Asp Gly Ser Pro Leu Phe
65 115 120 125
66 Tyr Ile Arg Lys Ile Leu Glu Thr Ile Phe Thr Ile Leu Phe Ala Phe
67 130 135 140
68 Tyr Leu Gln Tyr His Thr Tyr Tyr Leu Pro Ser Ala Ile Leu Met Gly
69 145 150 155 160
70 Val Ala Trp Gln Gln Leu Gly Trp Leu Ile His Glu Phe Ala His His
71 165 170 175
72 Gln Leu Phe Lys Asn Arg Tyr Tyr Asn Asp Leu Ala Ser Tyr Phe Val
73 180 185 190
74 Gly Asn Phe Leu Gln Gly Phe Ser Ser Gly Gly Trp Lys Glu Gln His
75 195 200 205
76 Asn Val His His Ala Ala Thr Asn Val Val Gly Arg Asp Gly Asp Leu
77 210 215 220
78 Asp Leu Val Pro Phe Tyr Ala Thr Val Ala Glu His Leu Asn Asn Tyr
79 225 230 235 240
80 Ser Gln Asp Ser Trp Val Met Thr Leu Phe Arg Trp Gln His Val His
81 245 250 255
82 Trp Thr Phe Met Leu Pro Phe Leu Arg Leu Ser Trp Leu Leu Gln Ser
83 260 265 270
84 Ile Ile Phe Val Ser Gln Met Pro Thr His Tyr Tyr Asp Tyr Tyr Arg
85 275 280 285
86 Asn Thr Ala Ile Tyr Glu Gln Val Gly Leu Ser Leu His Trp Ala Trp
87 290 295 300
88 Ser Leu Gly Gln Leu Tyr Phe Leu Pro Asp Trp Ser Thr Arg Ile Met
89 305 310 315 320
90 Phe Phe Leu Val Ser His Leu Val Gly Gly Phe Leu Leu Ser His Val
91 325 330 335
92 Val Thr Phe Asn His Tyr Ser Val Glu Lys Phe Ala Leu Ser Ser Asn
93 340 345 350
94 Ile Met Ser Asn Tyr Ala Cys Leu Gln Ile Met Thr Thr Arg Asn Met

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Output Set: N:\CRF4\07212003\I857583A.raw

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95          355          360          365
96 Arg Pro Gly Arg Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln
97          370          375          380
98 Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Thr
99          385          390          395          400
100 Val Met Pro Leu Val Lys Glu Phe Ala Ala Asn Gly Leu Pro Tyr
101          405          410          415
102 Met Val Asp Asp Tyr Phe Thr Gly Phe Trp Leu Glu Ile Glu Gln Phe
103          420          425          430
104 Arg Asn Ile Ala Asn Val Ala Ala Lys Leu Thr Lys Lys Ile Ala
105          435          440          445
107 <210> SEQ ID NO: 3
108 <211> LENGTH: 1275
109 <212> TYPE: DNA
110 <213> ORGANISM: Euglena gracilis
111 <400> SEQUENCE: 3
112 attttttttc gaaatgaagt caaagcgcca agcgctatcc cccttacaat tgatggaaca 60
113 aacatatgat gtggtcaatt tccaccctgg tgggtgcggaa attatagaga attaccaagg 120
114 aagggatgcc actgatgcct tcatggttat gcactttcaa gaagccttcg acaagctcaa 180
115 gcgcatgccc aaaatcaatc ccagttttga gttgccaccc caggctgcag tgaatgaagc 240
116 tcaagaggat ttccggaagc tccgagaaga gttgategea aetggeatgt ttgatgeete 300
117 cccctctggt tactcataca aaatcagcac cacactgggc cttggagtgc tgggttattt 360
118 cctgatgggt cagtatcaga tgtatttcat tggggcagtg ttgcttgga tgcactatca 420
119 acagatgggc tggctttctc atgacatttg ccaccaccag actttcaaga accggaactg 480
120 gaacaacctc gtgggactgg tatttgga caa tggctctgcaa ggtttttccg tgacatgttg 540
121 gaaggacaga cacaatgcac atcattcggc aaccaatggt caagggcacg accctgatat 600
122 tgacaacctc cccccccttag cctgggtctga ggatgacgtc acacgggcgt caccgatttc 660
123 ccgcaagctc attcagttcc agcagtacta tttcttggtc atctgtatct tgttgcggtt 720
124 catttggtgt ttccagtgcg tgttgaccgt gcgcagtttg aaggacagag ataaccaatt 780
125 ctatcgctct cagtataaga aggaggccat tggcctcgcc ctgcaactga ccttgaaggc 840
126 cctgttccac ttattcttta tgcccagcat cctcacatcg ctggttggtgt ttttcgtttc 900
127 ggagctggtt ggcggcttcg gcattgcgat cgtggtgttc atgaaccact acccaactga 960
128 gaagatcggg gacccagtct gggatggcca tggattctcg gttggccaga tccatgagac 1020
129 catgaacatt cggcgaggga ttatcacaga ttggtttttc ggaggcttga attaccagat 1080
130 tgagcaccat ttgtggccga cctccctcg ccacaacctg acagcggtta gctaccaggt 1140
131 ggaacagctg tgccagaagc acaacctgcc gtatcggaac ccgctgcccc atgaagggtt 1200
132 ggtcatcctg ctgcgctatc tggcggtgtt cgcccggatg gcggagaagc aaccgcggg 1260
133 gaaggtctta taagg 1275
135 <210> SEQ ID NO: 4
136 <211> LENGTH: 422
137 <212> TYPE: PRT
138 <213> ORGANISM: Euglena gracilis
139 <400> SEQUENCE: 4
140 Met Lys Ser Lys Arg Gln Ala Leu Ser Pro Leu Gln Leu Met Glu Gln
141 1 5 10 15
142 Thr Tyr Asp Val Ser Ala Trp Val Asn Phe His Pro Gly Gly Ala Glu
143 20 25 30
144 Ile Ile Glu Asn Tyr Gln Gly Arg Asp Ala Thr Asp Ala Phe Met Val
145 35 40 45

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Input Set : N:\Crf4\Refhold\I857583.raw

Output Set: N:\CRF4\07212003\I857583A.raw

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146 Met His Phe Gln Glu Ala Phe Asp Lys Leu Lys Arg Met Pro Lys Ile
147      50                      55                      60
148 Asn Pro Ser Phe Glu Leu Pro Pro Gln Ala Ala Val Asn Glu Ala Gln
149      65                      70                      75                      80
150 Glu Asp Phe Arg Lys Leu Arg Glu Glu Leu Ile Ala Thr Gly Met Phe
151                      85                      90                      95
152 Asp Ala Ser Pro Leu Trp Tyr Ser Tyr Lys Ile Ser Thr Thr Leu Gly
153                      100                      105                      110
154 Leu Gly Val Leu Gly Tyr Phe Leu Met Val Gln Tyr Gln Met Tyr Phe
155                      115                      120                      125
156 Ile Gly Ala Val Leu Leu Gly Met His Tyr Gln Gln Met Gly Trp Leu
157                      130                      135                      140
158 Ser His Asp Ile Cys His His Gln Thr Phe Lys Asn Arg Asn Trp Asn
159      145                      150                      155                      160
160 Asn Leu Val Gly Leu Val Phe Gly Asn Gly Leu Gln Gly Phe Ser Val
161                      165                      170                      175
162 Thr Cys Trp Lys Asp Arg His Asn Ala His His Ser Ala Thr Asn Val
163                      180                      185                      190
164 Gln Gly His Asp Pro Asp Ile Asp Asn Leu Pro Pro Leu Ala Trp Ser
165                      195                      200                      205
166 Glu Asp Asp Val Thr Arg Ala Ser Pro Ile Ser Arg Lys Leu Ile Gln
167      210                      215                      220
168 Phe Gln Gln Tyr Tyr Phe Leu Val Ile Cys Ile Leu Leu Arg Phe Ile
169      225                      230                      235                      240
170 Trp Cys Phe Gln Cys Val Leu Thr Val Arg Ser Leu Lys Asp Arg Asp
171                      245                      250                      255
172 Asn Gln Phe Tyr Arg Ser Gln Tyr Lys Lys Glu Ala Ile Gly Leu Ala
173                      260                      265                      270
174 Leu His Trp Thr Leu Lys Ala Leu Phe His Leu Phe Phe Met Pro Ser
175                      275                      280                      285
176 Ile Leu Thr Ser Leu Leu Val Phe Phe Val Ser Glu Leu Val Gly Gly
177      290                      295                      300
178 Phe Gly Ile Ala Ile Val Val Phe Met Asn His Tyr Pro Leu Glu Lys
179      305                      310                      315                      320
180 Ile Gly Asp Pro Val Trp Asp Gly His Gly Phe Ser Val Gly Gln Ile
181                      325                      330                      335
182 His Glu Thr Met Asn Ile Arg Arg Gly Ile Ile Thr Asp Trp Phe Phe
183                      340                      345                      350
184 Gly Gly Leu Asn Tyr Gln Ile Glu His His Leu Trp Pro Thr Leu Pro
185                      355                      360                      365
186 Arg His Asn Leu Thr Ala Val Ser Tyr Gln Val Glu Gln Leu Cys Gln
187      370                      375                      380
188 Lys His Asn Leu Pro Tyr Arg Asn Pro Leu Pro His Glu Gly Leu Val
189      385                      390                      395                      400
190 Ile Leu Leu Arg Tyr Leu Ala Val Phe Ala Arg Met Ala Glu Lys Gln
191                      405                      410                      415
192 Pro Ala Gly Lys Ala Leu
193                      420
195 <210> SEQ ID NO: 5

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## RAW SEQUENCE LISTING

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TIME: 09:49:11

Input Set : N:\Crf4\Refhold\I857583.raw

Output Set: N:\CRF4\07212003\I857583A.raw

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196 <211> LENGTH: 27
197 <212> TYPE: DNA
198 <213> ORGANISM: artificial sequence
199 <220> FEATURE:
200 <223> OTHER INFORMATION: PCR Primer
201 <220> FEATURE:
202 <221> NAME/KEY: misc_feature
203 <222> LOCATION: (12)..(12)
204 <223> OTHER INFORMATION: n = a, t, g, or c
205 <400> SEQUENCE: 5
W--> 206      ggctggctga cncaygartt ytgycay      27
208 <210> SEQ ID NO: 6
209 <211> LENGTH: 30
210 <212> TYPE: DNA
211 <213> ORGANISM: artificial sequence
212 <220> FEATURE:
213 <223> OTHER INFORMATION: PCR Primer
214 <220> FEATURE:
215 <221> NAME/KEY: misc_feature
216 <222> LOCATION: (13)..(13)
217 <223> OTHER INFORMATION: n = a, t, g, or c
218 <400> SEQUENCE: 6
W--> 219      catcgttgga aanarrtgrt gytcdatytg      30
221 <210> SEQ ID NO: 7
222 <211> LENGTH: 41
223 <212> TYPE: DNA
224 <213> ORGANISM: artificial sequence
225 <220> FEATURE:
226 <223> OTHER INFORMATION: PCR Primer
227 <400> SEQUENCE: 7
228      cccgggaagc ttctcgagga attttcaatc ctccttgggt c      41
230 <210> SEQ ID NO: 8
231 <211> LENGTH: 34
232 <212> TYPE: DNA
233 <213> ORGANISM: artificial sequence
234 <220> FEATURE:
235 <223> OTHER INFORMATION: PCR Primer
236 <400> SEQUENCE: 8
237      cccgggtgga tccggaacat atcacacgaa acag      34
239 <210> SEQ ID NO: 9
240 <211> LENGTH: 6
241 <212> TYPE: RNA
242 <213> ORGANISM: artificial sequence
243 <220> FEATURE:
244 <223> OTHER INFORMATION: Consensus sequence
245 <220> FEATURE:
246 <221> NAME/KEY: polyA_signal
247 <222> LOCATION: (1)..(6)
248 <223> OTHER INFORMATION:

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RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 07/21/2003  
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Input Set : N:\Crf4\Refhold\I857583.raw  
Output Set: N:\CRF4\07212003\I857583A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 12  
Seq#:6; N Pos. 13  
Seq#:12; Xaa Pos. 2,3  
Seq#:13; Xaa Pos. 2,3

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 2

VERIFICATION SUMMARY

DATE: 07/21/2003

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TIME: 09:49:12

Input Set : N:\Crf4\Refhold\I857583.raw

Output Set: N:\CRF4\07212003\I857583A.raw

L:206 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0  
L:219 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0  
L:249 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:0  
L:286 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0  
L:301 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0

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